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RAW SEQUENCE LISTING DATE: 12/06/2000
PATENT APPLICATION: US/09/715,249 TIME: 14:51:42

Input Set : A:\31192 Seq. Listing.txt
Output Set: N:\CRF3\12062000\I715249.raw

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      3 <110> APPLICANT: NOVARTIS AG
      4       VERES, GABOR
      5       PIPPIG, SUSANNE
      7 <120> TITLE OF INVENTION: selectable cell surface marker genes
      9 <130> FILE REFERENCE: 4-31192
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/715,249
C--> 11 <141> CURRENT FILING DATE: 2000-11-17
     11 <150> PRIOR APPLICATION NUMBER: us 60/166594
     12 <151> PRIOR FILING DATE: 1999-11-19
     14 <150> PRIOR APPLICATION NUMBER: us 09/539248
     15 <151> PRIOR FILING DATE: 2000-03-30
     17 <160> NUMBER OF SEQ ID NOS: 16
     19 <170> SOFTWARE: PatentIn version 3.0
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 3633
     23 <212> TYPE: DNA
     24 <213> ORGANISM: EGFR
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     31 ttgggcactt ttgaagatca tttctctcagc ctccagaagg tgttcaataa cctgtgaggtg   180
     33 gtccttggaa atttggaaat tacctatgtg cagaggaatt atgatctttc cttcttaaag    240
     35 accatccagg aggtggctgg ttatgtcctc attgccctca acacagtgga gcgaattcct    300
     37 ttggaaaacc tgcagatcat cagaggaaat atgtactacg aaaattccta tgccttagca    360
     39 gtcttatcta actatgatgc aaataaaacc ggactgaagg agctgcccat gagaaattta    420
     41 caggaaatcc tgcatggcgc cgtgcggttc agcaacaacc ctgccctgtg caacgtggag    480
     43 agcatccagt ggcgggacat agtcagcagt gactttctca gcaacatgtc gatggacttc    540
     45 cagaaccacc tgggcagctg ccaaaagtgt gatccaagct gtcccaatgg gagctgctgg    600
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     51 acaggccccc gggagagcga ctgcctggtc tgccgcaaat tccgagacga agccacgtgc    780
     53 aaggacacct gccccccact catgctctac aacccaacca cgtaccagat ggatgtgaac    840
     55 cccgagggca aatacagctt tggtgccacc tgcgtgaaga agtgtccccg taatttatgtg    900
     57 gtgacagatc acggctcgtg cgtccgagcc tgtgggggcg acagcctatga gatggaggaa    960
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     63 aactgcacct ccatcagtgg cgatctccac atcctgccgg tggcatttag gggtgactcc   1140
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     75 tttgggacct ccggtcagaa aaccaaaatt ataagcaaca gaggtgaaaa cagctgcaag   1500
     77 gccacaggcc aggtctgcca tgccttgtgc tccccgagg gctgctgggg cccggagccc    1560
     79 agggactgcg tctcttgccg gaatgtcagc cgaggcaggg aatgcgtgga caagtgcaag   1620
     81 cttctggagg gtgagccaag ggagtttgtg gagaactctg agtgcataca gtgccaccca   1680
     83 gagtgcctgc ctcaggccat gaacatcacc tgcacaggac ggggaccaga caactgtatc   1740
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 87 ggagaaaaca acaccctggt ctggaagtac gcagacgccg gccatgtgtg ccacctgtgc   1860
 89 catccaaact gcacctacgg atgcactggg ccagqtcttg aaggctgtcc aacgaatggg   1920
 91 cctaagatcc cgtccatcgc cactgggatg gtggggccc tcctcttgct gctggtggtg   1980
 93 gccctgggga tcggcctctt catgcgaagg cgccacatcg ttcggaagcg cacgctgcgg   2040
 95 aggctgctgc aggagaggga gcttgtggag cctcttacac cagtggaga agctcccaac   2100
 97 caagctctct tgaggatctt gaaggaaact gaattcaaaa agatcaaagt gctgggctcc   2160
 99 ggtgcgttcg gcacggtgta taagggactc tggatcccag aaggtgagaa agttaaaatt   2220
101 cccgtcgcta tcaaggaatt aagagaagca acatctccga aagccaacaa ggaaatcctc   2280
103 gatgaagcct acgtgatggc cagcgtggac aaccccacg tgtgccgcct gctgggcatc   2340
105 tgcctcacct ccaccgtgca actcatcacg cagctcatgc ccttcggctg cctcctggac   2400
107 tatgtccggg aacacaaaga caatattggc tcccagtacc tgctcaactg gtgtgtgcag   2460
109 atcgcaaagg gcatgaacta cttggaggac cgtcgcttgg tgcaccgcga cctggcagcc   2520
111 aggaacgtac tggtgaaaac accgcagcat gtcaagatca cagattttgg gctggccaaa   2580
113 ctgctgggtg cggaagagaa agaataccat gcagaaggag gcaaagtgcc tatcaagtgg   2640
115 atggcattgg aatcaatttt acacagaatc tatacccacc agaagtgatg ctggaggtac   2700
117 ggggtgaccg tttgggagtt gatgaccttt ggatccaagc catatgacgg aatcctgcc   2760
119 agcgagatct cctccatcct ggaggaaagga gaacgcctcc ctccagccacc catatgtacc   2820
121 atcgatgtct acatgatcat ggtcaagtgc tggatgataq acgcagataq tcgcccaaag   2880
123 ttccgtgagt tgatcatcga attctccaaa atggcccgag accccagcg ctaccttgtc   2940
125 attcagggag atgaaagaat gcatttgcca agtcctacag actccaactt ctaccgtgcc   3000
127 ctgatggatg aagaagacat ggacgacgtg gtggatgccg acgagtacct catcccacag   3060
129 cagggcttct tcagcagccc ctccacgtca cggactcccc tcctgagctc tctgagtgca   3120
131 accagcaaca attccaccgt ggcttgcatt gatagaaatg ggctgcaaag ctgtcccatc   3180
133 aaggaagaca gcttcttgca gcgatacagc tcagacccca caggcgcctt gactgaggac   3240
135 agcatagacg acaccttcct cccagtgcct gaatacataa accagtccgt tcccaaaagg   3300
137 ccccctggct ctgtgcagaa tcctgtctat cacaatcagc ctctgaaccc cgcgcccagc   3360
139 agagacccac actaccagga ccccacagc actgcagtgg gcaacccgga gtatctcaac   3420
141 actgtccagc ccacctgtgt caacagcaca ttcgacagcc ctgcccactg ggcccagaaa   3480
143 ggcagccacc aaattagcct ggacaaccct gactaccagc aggacttctt tcccaaggaa   3540
145 gccaagccaa atggcatctt taagggctcc acagctgaaa atgcagaata cctaagggtc   3600
147 gcgccacaaa gcagtgaatt tattggagca tga                                3633
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151 <211> LENGTH: 1210
152 <212> TYPE: PRT
153 <213> ORGANISM: EGFR
155 <400> SEQUENCE: 2
157 Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
158 1               5                   10                  15
160 Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
161             20                  25                  30
163 Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
164         35                  40                  45
166 Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
167     50                  55                  60
169 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
170 65                  70                  75                  80
172 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
173                 85                  90                  95
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175 Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
176             100                 105                 110
178 Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
179         115                 120                 125
181 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
182     130                 135                 140
184 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
185 145                 150                 155                 160
187 Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
188                 165                 170                 175
190 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
191             180                 185                 190
193 Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Glu
194         195                 200                 205
196 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
197     210                 215                 220
199 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
200 225                 230                 235                 240
202 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
203                 245                 250                 255
205 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
206             260                 265                 270
208 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
209         275                 280                 285
211 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
212     290                 295                 300
214 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
215 305                 310                 315                 320
217 Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
218                 325                 330                 335
220 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
221             340                 345                 350
223 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
224         355                 360                 365
226 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
227     370                 375                 380
229 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
230 385                 390                 395                 400
232 Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
233                 405                 410                 415
235 Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
236             420                 425                 430
238 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
239         435                 440                 445
241 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
242     450                 455                 460
244 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
245 465                 470                 475                 480
247 Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
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248                 485                 490                 495
250 Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
251             500                 505                 510
253 Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
254         515                 520                 525
256 Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
257     530                 535                 540
259 Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
260 545                 550                 555                 560
262 Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
263                 565                 570                 575
265 Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
266             580                 585                 590
268 Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
269         595                 600                 605
271 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
272     610                 615                 620
274 Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
275 625                 630                 635                 640
277 Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
278                 645                 650                 655
280 Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
281             660                 665                 670
283 Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
284         675                 680                 685
286 Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Glu Ala Leu Leu
287     690                 695                 700
289 Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
290 705                 710                 715                 720
292 Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
293                 725                 730                 735
295 Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
296             740                 745                 750
298 Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
299         755                 760                 765
301 Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
302     770                 775                 780
304 Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
305 785                 790                 795                 800
307 Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
308                 805                 810                 815
310 Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
311             820                 825                 830
313 Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
314         835                 840                 845
316 Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
317     850                 855                 860
319 Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
320 865                 870                 875                 880
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322 Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
323                 885                 890                 895
325 Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
326             900                 905                 910
328 Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
329         915                 920                 925
331 Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
332     930                 935                 940
334 Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
335 945                 950                 955                 960
337 Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
338                 965                 970                 975
340 Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
341             980                 985                 990
343 Thr Asp Ser Asn Phe Tyr Arg Ala  Leu Met Asp Glu Glu  Asp Met Asp
344         995                 1000                1005
346 Asp Val  Val Asp Ala Asp Glu  Tyr Leu Ile Pro Gln  Gln Gly Phe
347     1010                1015                1020
349 Phe Ser  Ser Pro Ser Thr Ser  Arg Thr Pro Leu Leu  Ser Ser Leu
350     1025                1030                1035
352 Ser Ala  Thr Ser Asn Asn Ser  Thr Val Ala Cys Ile  Asp Arg Asn
353     1040                1045                1050
355 Gly Leu  Gln Ser Cys Pro Ile  Lys Glu Asp Ser Phe  Leu Gln Arg
356     1055                1060                1065
358 Tyr Ser  Ser Asp Pro Thr Gly  Ala Leu Thr Glu Asp  Ser Ile Asp
359     1070                1075                1080
361 Asp Thr  Phe Leu Pro Val Pro  Glu Tyr Ile Asn Gln  Ser Val Pro
362     1085                1090                1095
364 Lys Arg  Pro Ala Gly Ser Val  Gln Asn Pro Val Tyr  His Asn Gln
365     1100                1105                1110
367 Pro Leu  Asn Pro Ala Pro Ser  Arg Asp Pro His Tyr  Gln Asp Pro
368     1115                1120                1125
370 His Ser  Thr Ala Val Gly Asn  Pro Glu Tyr Leu Asn  Thr Val Gln
371     1130                1135                1140
373 Pro Thr  Cys Val Asn Ser Thr  Phe Asp Ser Pro Ala  His Trp Ala
374     1145                1150                1155
376 Gln Lys  Gly Ser His Gln Ile  Ser Leu Asp Asn Pro  Asp Tyr Gln
377     1160                1165                1170
379 Gln Asp  Phe Phe Pro Lys Glu  Ala Lys Pro Asn Gly  Ile Phe Lys
380     1175                1180                1185
382 Gly Ser  Thr Ala Glu Asn Ala  Glu Tyr Leu Arg Val  Ala Pro Gln
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386     1205                1210
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389 <211> LENGTH: 31
390 <212> TYPE: DNA
391 <213> ORGANISM: primer
393 <400> SEQUENCE: 3
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VERIFICATION SUMMARY DATE: 12/06/2000
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Input Set : A:\31192 Seq. Listing.txt
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date